F - G - A

MATCH WITH FIG. 1E

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GTGCTGTACCTCCCCCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT

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GCCAGCCCTCAACACCTCTTTCTGCTGGGCTGCTGGCAACGCCGCGGTGCAGC	CGTGCTGCTGAGCGGCGCACCCTTCCTGCTCCACCTAGC CGTGCTGCTGAGCCGGCGGCACCCTGAGCAGCACCCTCGACCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACCACCTTCCTGCTCCACCTAGC CGTGCTGCTGAGCCGGCGACAGCCCTGAGCAGCACCGACCACCTTCCTGCTCCACCTTAGC CGTGCTGCTGAGCCGGCGGCACCCTGAGCAGCACCGACCACCTTAGCTAGC	630 TGTAGCAGACACTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA TGTAGCAGACACGCTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCTGCTCACACTGCCGCTCCTGGACGCTGCTGCTCACACTGCCGCTCTGGGCAGTGGACGCTGCTCACACTACAAAAAAAA	GTGGGTCTTTGGCTCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA M V F G S G L C K V A G A L F N I N F Y	750 730 CGCAGGAGCCCTCCTGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC	A G A L L T C L A V W CACCCAGCTCACCTGCCTGGCTGTCTG	TOLYRRGP890 850 8GGCTCTGCCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA	G L C L L F A L P D F F F 950 930 910 GCGCTCAACGCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGCTTGCG	H C O Y N F F K
GCCAGCCTCAACAGCCTCCTCTTTCTGC	CGTGCTGCTGAGCCGGCGGACAGCCCTG	610 TGTAGCAGCTGCTGGTGCTGAC	670 GTGGGTCTTTGGCTCTGGCAA W F G S G L C K	CGCAGGAGCCCTCCTGCTGCAT	A G A L L L 790 790 CACCCAGCTCTACCGCGGGGGCCCC	T Q L Y R R G F F 850 GGGCTCTGCCTGTTTTCGCCTCC	G L C L L F A L P 910 GCGCCTCAACGCCACCCACTGCCAAT	B L N A T H C Q

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	GGTGCTGCAGCTGGTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC	A,	>	GGCCGTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT	J	-	GGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT	· 山	•	CCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT	>		AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT	KSVTSGLGYMHCCLNPL	
	CTZ	⊁		CCC	ĸ		GGJ	>		CAG	ĸ		CCC	Д	
	CTG	ပ		CAT	Σ		GGT	>	•	AAG	ß		CAA	Z	
1010	CTA	7	1070	CGC	A	1130	CCT	J	1190	AGA	्ध	1250	CCT	Ä	1310
10	CGC	A	10	CCG	K	11	TCA	H	11	CCG	Ä	12	CTG	ບ	13
•	CAT	Σ		CCT	ר		CTA	X		TGG	Ö		CTG	Ö	
	GGT	>		SCG	. K		CCC	Ь	-	CTG	Ö		GCA	H	•
	GCT	'n		SCG	8		GAC	H	•	CAA	z		CAT	Σ	
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990	GCT	LVAGFLLPLLVMAYCYA	1050	CAG	AVLLVSRGQRRLRAMRL	1110	CCT	V V V A F, A L C W T P Y H L V V	1170	$ ext{TTT}$	LMDLGALARNCGRESRV	1230	CCT	IJ	1290
	TCT	J	 1	TTC	ώ	~	TGC	K	. –	CGC	A	Н	AGG	Ö	Н
?	CTT	· [14	÷	GGT	>	٠.	CTT	[T,	,	GGG	Ö		CTC	ß	
	$\overline{\mathrm{TGG}}$	Ŋ		GCT	ı		GGC	K		CCT	T		CAC	Ę	
	CGC	A		GCT	H		GGT	>		GGA	Ω		GGT	>	
	GGT	>		CGT	>		CGT	>		CAT	Σ		GTC	ß	
0	GCT	T	0	CGC	K	0	GGT	>	0	CCT	L	0	CAA	×	
97	GCA	Ø	103	CCT	H I L	109	GGT	A A A	115	CAT	V D I	121	CCC	A.	127(
	GCT	V L Q		CAT	Н		GGT	>		GGA	Ω		CGT	A V O	
	GGT	>.		CCACATCCT	H		GGT	>	٠.	GGTGGACAT	>		AGA	Ò	. (

MATCH WITH FIG. 1D

GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT

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1350	GGGCTGCCCCAACCAGAGAGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC	G C P N Q R G L Q R Q P S S S R R D S S	1410	CTGGTCTGAGACCTCAGAGGÇCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC	TSEASYSGL*	1470	AGTCTGACTTCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG	1530	TATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCAGGTCTCCC	1590	CCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC	1650	CCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA	1710 1730	CCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA	1770	CAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT	1830	ATTTGGTCTTTTTTTTTTTGTCTAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG	
1330	GGGCTGCCCCAACCAGAGA	G C P N Q R	1390	CTGGTCTGAGACCTCAGAC	W S E T S E	1450	TTTCGCCCACAGTCTGAC	1510	CTCTCCCCAATATCCTCG	1570	GGGAAGCCACCCTCCCAG	1630	CATCCTGCCGCCCGAGGTC	1690	ACTTCATCTTCCCCAAGTC	1750	AGCCACAGCCCAGGCCTCC	1810	ATTTGGTCTTTTATTTTT	1870

TCAGGAAAAAAAAAA

F1G.2A

103	46	153	96	203	146	253	195	301	245	
54 DHOVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFL	2 ESDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPCEPESLEINKYFV	104 PALASLLFLIGLIGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTL	47 VIIYALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTL	154 PLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHA	- .	204 TOLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYN		254 FPQVG. RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAM	196 GNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQKHRAM	MATCH WITH FIG 2B
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SUBSTITUTE SHEET (RULE 26)

MATCH WITH FIG. 2A

302 RLVV	302 RLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
246 RVIFAVV	AVVLIFILCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE 295
352 GLGY	GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRD 401
•	
296 ILGI	ILGILHSCLNPLIYAFIGOKFRHGLLKILAIHGLISKDSLPKDSRPSFVG 345
402 SSWS	SSWSETSEA 410
346 SSSGHTS	HTSTT 354

SUBSTITUTE SHEET (RULE 26)





IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

SUBMISSION OF SUBSTITUTE FORMAL DRAWINGS

Commissioner for Patents Washington, D.C. 20231

To the Official Draftsperson:

Applicants submit herewith Substitute Formal Drawings of Figures 1A-1D and 2A-2B (six sheets) to replace the previously filed drawings of Figures 1A-1D and 2A-2B (six sheets). The enclosed drawings have been amended to correspond to the sequences shown in the Substitute Sequence Listing filed herewith, as discussed in detail in the Response and Amendment also filed herewith.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: March 18, 2002

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(Reg. No. 46,789)

Attorney for Applicants

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9410 Key West Avenue Rockville, MD 20850

(240) 314-1224

Enclosures KKH/MJH/KC/mlm

FIG. 1A

130 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT	MEL	190 210 230	GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA	R K Y G P G R L A G T V I G G A A Q S K	250 270 290	ATCACAGACTAAATCAGACTCAAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC	SOTKSDSITKEFLPGLYTAP	310 330 350	TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT	SSPFPSQVSDHQVLNDAEV	370 390 410	TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC	A A L L E N F S S Y D Y G E N E S D S	430 450 470	GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	30 30 310 310 110 90 1110 110 110 110 110 110 110 1
GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG	GACGCTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGATGAGATGCGAG	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT MELL 190	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCCAGACTGAGCGGATGGAGTT M E L 210 AGAGGAAGTACGGCCCTGGAAGACTGGCGGGACAGTTATAGGAAGGA	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 AGAAGCAGCTTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT M E L 210 230 GAGGAAGTACGGCCCTGGAAGACTGGCGGACGACTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT M E L 230 AGGGAAGTACGGCCCTGGAAGACTGGCGGGACAGTTATAGGAGGAGCTCCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 250	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 AGAAGCAGCTTTGAGAAGGAAGTCACTATCCCAGACCCAGACTGAGCGGATGGAGTT 190 210 210 230 R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 AGAAGCAGCTTTTGAGAAGGGAAGTCACTATCCCAGACCCAGACTGAGCGGATGGAGTT 190 210 210 230 R K Y G P G R L A G T V I G G A A Q S K 250 270 270 ATCACAGACTAAATCAGACTCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGACCCAGACTGAGCGGATGGAGTT 190 210 210 230 R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAATCAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 270 270 ATCACAGACTAAATCAGACTCAATCAAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 330	GACGCTCTTCTTCCTGCCCAGGGGTCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 130 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGACCCAGACTGAGCGGATGGAGTT 190 CAGGAAGTACGGCCCTGGAAGACTGGCGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P P TTCCTCCCGGTTCCCGCCCTCACAGGTGACCACCCAAGTGCTAAATGACGCCGAGGT	GACGCTCTTCTTCCTGCCCAGGGGTCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 AGAAGCAGCCTTTGAGAAGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 190 GAGGAAGTACGGCCCTGGAAGACTCGCGGGACAGTTATAGGAGGAGCTCCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCCTCACAGGTGACTGACCAAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 170 AGAAGCAGCTTTTGAGAAGTCACTATCCCAGACCCCAGACTGAGCGGATGGAGTT 190 CAGGAAGTACGCCCTGGAAGACTGGCGGGACAGTTATAGGAGGACTGCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P S 310 TTCCTCCCCGTTCCCGCCCTCACAGGTGACTGACCACAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 370	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGACCCAGACTGAGCAGTT M E L 190 GAGGAAGTACGGCCCTGGAAGATCACTATCCCAGACTGAGCGGTTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGAATCACAAAAGAGTTCCTGCCAGGCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCTCACAGGTGACTGACTCAAATGACGCCGAGGT S Q T R S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCCTCACAGGTGACTGACTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCCTCCTGGAGAACTTCCAGCTCTTCCTATGGAGAAAACGAGAGTGACTC	GACGCTCTTCTTCCTGCCCAGGGGTCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 AGAAGCAGCCTTTGAGAAGGTCACTATCCCAGAGCCCAGACTGAGCTT M E L 210 230 AR K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAATCAGACTCAAAAAGATTCCTGCCAGACTTTACACAGCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCGTTCCCGCCTCAAAAGAGTTCCTGCCAGGCCTTTACACAGCCC S Q V S D H Q V L N D A E V 370 TGCGCCCTCGAAGACTTCCTATGACTATGAAGGTTCCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCTCTGGAAACTTCCTATGACTATTGAAAAGAAACGAAAACGAAAACTC A L L E N F S S Y D Y G E N E S D S	GACGCTCTTCTTCCTGCCCAGGGGTCCTTGGGCCGATGGGATCACGCAGAAGAATGCGAG 130 150 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGACCCAGACTGAGCGGATGGAGTT 190 GAGGAAGTACGGCCCTGGAAGACTGCCGGGGACAGTTATAGGAGCGGATGAGTTA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAAATCACAAAAGAGTTCCTGCCAGGCTTTACACAGCCC S Q T K S D S I T K E F L P G L Y T A P 310 330 TTCCTCCCCGTTCCCGCCTCACAGGTGACTGACTCAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCTTCCAGAGACTTCCAAGGTGACTAAATGACGCCGAGGT A A L L E N F S S Y D Y G E N E S D S 430 4410	10 CCTGAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
	130 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT	130 AGAAGCAGCCTTTGAGAAGGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT M E L	150 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT M E L 190	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT M E L 230 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGGAGCTCAGAGTAA	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT M E L M E L 210 230 R K Y G P G R L A G T V I G G A A Q S K	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT MELL 210 230 230 AGAGGAAGTACGGCCCTGGAAGACTGGCGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 250	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 190 230 230 R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGAAAAAGAGTTCCTGCCAGGCCTTTACAGGCCCCCCC	AGAAGCAGCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 190 210 230 R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAAAAAGAGTTCCTGCCAGGCCTTTAACACAGCCCC 2 90 2 7	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 190 210 230 R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 310	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 190 210 230 R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGATCACTACAAAAGAGTTCCTGCCCAGGCCTTTACACGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCGGTTCCCGCCTCAAGGTGACCACCAAGTGCTAAATGACGCCGAGGT	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 190 CAGGAAGTACGCCCTGGAAGACTGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCACAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCCTCACAGGTGACTGACCAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 190 GAGGAAGTACGGCCCTGGAAGACTGGCGGGACAGTTATAGGAGGACTCCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 ATCCTCCCGGTTCCCGCCCTCACAGGTGACTGACCACCCCAAGTGCTAAATGACGCCCGAGGT TTCCTCCCCGTTCCCGCCCTCACAGGTGACTGACCACAAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 370 410	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCGACTGAGCGGATGGAGTT 190 CAGGAAGTACGGCCCTGGAAGACTCGCGGGACAGTTATAGGAGGAGCTCCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAATCACAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCCTCAGGTGAGTGACCCCCAAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCTCCTGGAGAACTTCAGCTCTTCCTATGAGAAAACGAGAGTGACTC	AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCAGACTGAGCGGATGGAGTT 190 GAGGAAGTACGGCCTGGAAGACTGGCGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCGTTCCCGCTCAAAAGAGTGACCAAGTGCTAAATGACGCCGAGGT S S P F P P S Q V S D H Q V L N D A E V 370 TGCCGCCCTCCTGGAGAACTTCCTATGAGAAAAAGAGAGACTC A A L L E N F S S Y D Y G E N E S D S	AGAAGCAGCCTTTGAGAAGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGTTGAGGAGTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGGAGTTTTTGAGAAGGATTATAGGAGGAGCTCAGAGTAAA R L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L A G T V I G G A A Q S K L L CACAGACTCAAAACAAAAGAGTTCCAAAAAGAGTTCCTGCCAGGCTTACCAGGTGACTCAAAAAGAGTGACTCAAAAAGAGAGAG	GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGGATCACGCAGAAGAATGCGAG
GAGGAAGTACGGCCCTGGAAGACTGGCGGGACCAGTTATAGGAGGAGCTCCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCCTCACAGGTGACTGACCAAGTGCTAAATGACGCCGAGGT S P F P P S Q V S D H Q V L N D A E V 370 TGCCGCCCTCCTGGAGAACTTCCTATGACTATGGAGAAACGAGAGTGACTC A A L L E N F S S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCGCCCTCCCACAGGACTTCCAGGCCTTCCT	190 GAGGAAGTACGGCCCTGGAAGACTGCCGGGGACCGTTATAGGAGGACTCCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCCTCACAGGTGACCACCCAAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCTCCTGGAGAACTTCCTATGACTATGGAGAAAACGAGACTC A A L L E N F S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCGCCCTCACAGGACTTCCAGGCCTTCCT	GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCGGTTCCCGCCCTCACAGGTGAGTGACCACGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCTCCTGGAGAACTTCAGCTCTTCCTATGAGAAACGAGAGTGACTC A A L L E N F S S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCGGCCCTGCCAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	R K Y G P G R L A G T V I G G A A Q S K 250 ATCACAGACTAAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 310 TTCCTCCCCGTTCCCGCCCTCACAGGTGACTACCAAGTGCTAAATGACGCCGAGGT S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGAGAAAACGAGAGTGACTC A L L E N F S S Y D Y G E N E S D S GTGCTGTACCTCCCCCCTCCCCCCCCCCCCCCCCCCCCC	250 270 270 290 ATCACAGACTAAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S T K S D S I T K E F L P G L Y T A P 330 310 310 TTCCTCCCGTTCCCGCCCTCACAGTGAGTGACCACCCAAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 390 TGCCGCCTTCTGGAGAACTTCAGCTCTTTCCTATGACTATGGAGAAACGAGAGTGACTC A L L E N F S S Y D Y G E N E S D S GTGCTGTACCTCCCCGCCCTCCCGCCCTCCCGGAGACTTCAGGCTTCAGCCTTCCTATGACTTCGACCGGGCCTTCCT	ATCACAGACTAAATCAGACTCAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC S Q T K S D S I T K E F L P G L Y T A P 330 310 310 370 TCCTCCCCGTTCCCGCCCTCACAGGTGACTGACCACAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCCTCCTGGAGAACTTCCTATGACTATGAGAAAACGAGAGTGACTC A A L L E N F S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	S Q T K S D S I T K E F L P G L Y T A P 330 310 TTCCTCCCGCTCCACAGGTGACCACCAAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 390 TGCCGCCTCCTGAGAACTTCAGCTCTTCCTATGACAAACGAGAGTGACTC A A L L E N F S S Y D Y G E N E S D S 410 430 GTGCTGTACCTCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	310 310 330 350 TTCCTCCCCGCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGAGAAAACGAGAGTGACTC A L L E N F S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCGCCCTGCCCAGGACTTCAGCCTTCCT GTGCTGTACCTCCCGCCCTGCCCACAGGACTTCAGCCTTCCT	TTCCTCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT S S P F P S Q V S D H Q V L N D A E V 370 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAACGAGAGTGACTC A A L L E N F S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	S S P F P S Q V S D H Q V L N D A E V 390 410 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC A A L L E N F S S Y D Y G E N E S D S 430 450 450 470 GTGCTGTACCTCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	370 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC A L L E N F S S Y D Y G E N E S D S 430 470 GTGCTGTACCTCCCGCCCTGCCCACAGGACTTCAGCCTGAAACGAGAGTGACTCCT	TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC A L L E N F S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	A A L L E N F S S Y D Y G E N E S D S 430 GTGCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	430 450 GIGCTGTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT	GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT		C C T S P P C P Q D F S L N F D R A F L

FIG. 1B

490 GCCAGCCCTCTTTTCTGGGGCTGCTGGCAACGGCGGTGGCAGC PALYSLLFLGGLGGCTGCTGGCAACGGCGGTGGCAGC FALYSLLFGGGGCTGCTGGGCAACGGCGGTGGCAGC FALYSLLFGGGGCTGCTGGGAACGGCGGTGGCAGC	CGTGCTGCTGAGCCGGCGGACAGCCTGGCACCGACACCTTCCTGCTCCACCTAGC V L L S R R T A L S S T D T F L L H L A 630 630	TGTAGCAGACACGCTGCTGGTGCTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA V A D T L L V L T L P L W A V D A A V Q 670	GTGGGTCTTTGGCTCTGGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA W V F G S G L C K V A G A L F N I N F Y 730	CGCAGGAGCCCTCCTGCTGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC A G A L L L A C I S F D R Y L N I V H A 790 830	CACCCAGCTCTACCGCCCGGGGCCCCGGCCGTGACCCTCACCTGCCTG	CTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA
490 GCCAGCCTCTACAGCCTCC P A L Y S L I 550	CGTGCTGCTGAGCCGGCGGAV V L L S R T 610	TGTAGCAGACGCTGCTGC V A D T L L V 670	GTGGGTCTTTGGCTCTGGCC W V F G S G I 730	CGCAGGAGCCCTCCTGCTGG A G A L L L L 7	CACCCAGCTCTACCGCCGGC T Q L Y R R G 850	GGGCTCTGCCTGCTTTTCG

FIG. 1C

950	GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG	PQVGRTALR	1010	CCTGCTGGTCATGGCCTACTGCTATGC	LLVMAYCYA	1070	CCAGCGCCCTGCGGGCCATGCGGCT	Q R R L R A M R L	1130	GGTGGTGGTCGTGGTGGCCTTTGCCCTTCTGCTGGACCCCCTATCACCTGGTGGTGCT	W T P Y H L V V L	1190	CCGCAACTGTGGCCGAGAAAGCAGGGT	R N C G R E S R V	1250	AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT	Y M H C C L N P L	1310	GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT	RMWMLLLRL
930	ACTGCCAATACAACTT	I C Q Y N F	066	CTGGCTTTCTGCTGCC	G F L L P	1050	TGCTGGTTTCCAGGGG	LVSRG	1110	HGGCCTTTGCCCTCTG	7 A F A L C	1170	*ACCTGGGCGCTTTGGCC) L G A L A	1230	HCACCTCAGGCCTGGG	7 T S G L G	1290	GGGTCAAGTTCCGGGA (JVKFRE
910	GCGCCTCAACGCCACCC	R L N A T H	970	GGTGCTGCAGCTGGTGG	VLQLVA	1030	CCACATCCTGGCCGTGC	H I L A V I	1090	GGTGGTGGTCGTGG		1150	GGTGGACATCCTCATGG	V D I L M I	1210	AGACGTGGCCAAGTCGG	D V A K S V	1270	GCTCTATGCCTTTGTAG	LYAFVG

FIG. 1D

1330 1350 . 1370
GGGCTGCCCCAACCAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC G C P N Q R G L Q R Q P S S S R R D S S 1410
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1450 1470 1490
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1510 1530 1550
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1570 1590 1610
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1630 1650 1670
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1870
TCAGGAAAAAAAA

F1G2A

KYFV 46 VLTL 153	IVHA 20.	CQYN 25	LRAM 30
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APCEPE STDTFLLH	AGALLLAC SGILLLAC	FIFLSAHH LLFRRTVY	YAHILAVI YGFTLRTI
PPFLLDA!	ALFNINFY.	CLLFALPD	PLLVMAYC
NYSYSSTE GAVAAVLE	GLCKVAGP : FLCKVVSI	CLAVWGLC CLSIWGLS	LVAGFLLH
WKGEDLSI LLGLLGN	VQWVFGS . . NGWIFGT	PARVTLT	TALRVLO
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2 1 2 1 104 1	154]	204	254

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

STATEMENT UNDER 37 C.F.R. §§1.821 AND 1.825

Commissioner for Patents Washington, D.C. 20231

Sir:

Pursuant to 37 C.F.R. §§1.821(f) and 1.825(b), Applicants hereby certify that the sequence listing information recorded in computer readable form and submitted herewith is identical to the written (on paper) Substitute Sequence Listing submitted herewith.

Applicants further certify under 37 C.F.R. §§1.821(g) and 1.825(a) that the Substitute Sequence Listing submitted herewith contains no new matter.

Respectfully submitted,

Dated: March 18, 2002

Mark J. Hyman

Reg. No. 46,789

Attorney for Applicants

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Enclosures KKH/MJH/KC

SEQUENCE LISTING

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gac	gctc	ttc 1	tcct	gcc	ca go	gggto	ccct	g ggo	ccgat	ggg	atca	acgca	aga a	agaat	tgcgag	120
agaa	agca	gcc 1	ttga	agaaq	gg ga	aagto	cacta	a tco	ccaga	agcc	caga	actga	agc (tg gag et Glu	178
		aag Lys 5														226
		cag Gln														274
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		cca Pro														
Phe 35 cag	Leu gtg		Gly gac	Leu	Tyr 40 caa	Thr gtg	Ala	Pro aat	Ser gac	Ser 45 gcc	Pro	Phe gtt	Pro	Pro	Ser 50 ctc	370



																b 4.	;	
								tgc Cys 90									466	
	_		_				_	ctc Leu		_					_	ggg Gly	514	
								gca Ala									562	
	-	_	_	_		_		ttc Phe	_				-	-	_	_	610	
	_		_		_		_	ccg Pro			_		_	_	_	_	658	
	_		_					ctc Leu 170	Cys			-		-			706	
						_		gcc Ala		_	_	_	_		_		754	
~~	-	-		_			-	cat His	-		-			_			802	
Cont.			-					acc Thr	-	_	-	_				-	850	
				-			_	ttc Phe			_	_	-			-	898	
								tgc Cys 250									946	
								cag Gln									994	
								tat Tyr									1042	
								ctg Leu									1090	
								tgc Cys									1138	

·	
ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc aac tgt ggc Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn Cys Gly 325 330 335	1186
cga gaa agc agg gta gac gtg gcc aag tcg gtc acc tca ggc ctg ggc Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly Leu Gly 340 345 350	1234
tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt gta ggg gtc Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val Gly Val 355 360 365 370	1282
aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg ggc tgc ccc Lys Phe Arg Glu Arg Met Trp Met Leu Leu Arg Leu Gly Cys Pro 375 380 385	1330
aac cag aga ggg ctc cag agg cag cca tcg tct tcc cgc cgg gat tca Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg Asp Ser 390 395 400	1378
tcc tgg tct gag acc tca gag gcc tcc tac tcg ggc ttg tga Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu 405 410 415	1420
ggccggaatc cgggctcccc tttcgcccac agtctgactt ccccgcattc caggctcctc	1480
cctccctctg ccggctctgg ctctccccaa tatcctcgct cccgggactc actggcagcc	1540
ccagcaccac caggtetece gggaagecae ecteecaget etgaggaetg caccattget	1600
getecttage tgecaagece cateetgeeg eeegaggtgg etgeetggag eeecactgee	1660
cttctcattt ggaaactaaa acttcatctt ccccaagtgc ggggagtaca aggcatggcg	1720
tagagggtgc tgccccatga agccacagcc caggcctcca gctcagcagt gactgtggcc	1780
atggtcccca agacctctat atttggtctt ttatttttat gtctaaaatc ctgcttaaaa	1840
cttttcaata aacaagatcg tcaggaaaaa aaaaaa	1876

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<211> 415

<212> PRT

<213> Homo sapiens

<400> 2

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Gly Gly Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr 20 25 30

Lys Glu Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro 35 40 45

Pro	Ser 50	Gln	Val	Ser	Asp	His 55	Gln	Val	Leu	Asn	Asp 60	Ala	Glu	Val	Ala
Ala 65	Leu	Leu	Glu	Asn	Phe 70	Ser	Ser	Ser	Tyr	Asp 75	Tyr	Gly	Glu	Asn	Glu 80
Ser	Asp	Ser	Cys	Cys 85	Thr	Ser	Pro	Pro	Cys 90	Pro	Gln	Asp	Phe	Ser 95	Leu
Asn	Phe	Asp	Arg 100	Ala	Phe	Leu	Pro	Ala 105	Leu	Tyr	Ser	Leu	Leu 110	Phe	Leu
Leu	Gly	Leu 115	Leu	Gly	Asn	Gly	Ala 120	Val	Ala	Ala	Val	Leu 125	Leu	Ser	Arg
Arg	Thr 130	Ala	Leu	Ser	Ser	Thr 135	Asp	Thr	Phe	Leu	Leu 140	His	Leu	Ala	Val
Ala 145	Asp	Thr	Leu	Leu	Val 150	Leu	Thr	Leu	Pro	Leu 155	Trp	Ala	Val	Asp	Ala 160
Ala	Val	Gln	Trp	Val 165	Phe	Gly	Ser	Gly	Leu 170	Cys	Lys	Val	Ala	Gly 175	Ala
Leu	Phe	Asn	Ile 180	Asn	Phe	Tyr	Ala	Gly 185	Ala	Leu	Leu	Leu	Ala 190	Cys	Ile
Ser	Phe	Asp 195	Arg	Tyr	Leu	Asn	Ile 200	Val	His	Ala	Thr	Gln 205	Leu	Tyr	Arg
Arg	Gly 210	Pro	Pro	Ala	Arg	Val 215	Thr	Leu	Thr	Cys	Leu 220	Ala	Val	Trp	Gly
Leu 225	Cys	Leu	Leu	Phe	Ala 230	Leu	Pro	Asp	Phe	Ile 235	Phe	Leu	Ser	Ala	His 240
His	Asp	Glu	Arg	Leu 245	Asn	Ala	Thr	His	Cys 250	Gln	Tyr	Asn	Phe	Pro 255	Gln
Val	Gly	Arg	Thr 260	Ala	Leu	Arg	Val	Leu 265	Gln	Leu	Val	Ala	Gly 270	Phe	Leu

Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val 275 280 285

Leu Le 29		Ser	Arg	Gly	Gln 295	Arg	Arg	Leu	Arg	Ala 300	Met	Arg	Leu	Val`		
Val Va 305	l Val	Val	Val	Ala 310	Phe	Ala	Leu	Cys	Trp 315	Thr	Pro	Tyr	His	Leu 320	•	ı
Val Va	l Leu	Val	Asp 325	Ile	Leu	Met	Asp	Leu 330	Gly	Ala	Leu	Ala	Arg 335	Asn		
Cys Gl	y Arg	Glu 340	Ser	Arg	Val	Asp	Val 345	Ala	Lys	Ser	Val	Thr 350	Ser	Gly		
Leu Gl	y Tyr 355	Met	His	Cys	Cys	Leu 360	Asn	Pro	Leu	Leu	Tyr 365	Ala	Phe	Val		
Gly Va 37	_	Phe	Arg	Glu	Arg 375	Met	Trp	Met	Leu	Leu 380	Leu	Arg	Leu	Gly		
Cys Pr 385	o Asn	Gln	Arg	Gly 390	Leu	Gln	Arg	Gln	Pro 395	Ser	Ser	Ser	Arg	Arg 400		
Asp Se	r Ser	Trp	Ser 405	Glu	Thr	Ser	Glu	Ala 410	Ser	Tyr	Ser	Gly	Leu 415			
<210><211><211><212><213>	3 29 DNA Arti	ficia	al se	equei	nce											
<220> <223>	Cont	ains	a Ba	amHI	rest	crict	cion	enzy	yme s	site						
<400> cgggat	3 cctc	catgo	gagt	tg a	ggaaq	gtac										29
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<220>
<223> Contains a HindIII site
gtccaagctt gccaccatgg agttgaggaa gtac
                                                                     34
<210> 6
<211>
      57
<212>
      DNA
<213> Artificial sequence
<220>
<223> Contains complementary sequences to a XhoI site, translation stop
       codon, and an HA tag
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ctgctcgagt caagcgtagt ctgggacgtc gtatgggtag cacaagcccg agtagga
                                                                     57
<210> 7
<211> 31
<212> DNA
<213> Artificial sequence
<220>
<223> Contains a BamHI restriction enzyme site followed by 5 nucleotide
       s resembling an efficient signal for the initiation of translatio
       n in eukaryotic cells (J. Mol. Biol. 1987, 196, 947-950, Kozak, M
       .)
<400> 7
cgggatccct cccatggagt tgaggaagta c
                                                                     31
<210> 8
<211> 29
<212> DNA
<213> Artificial sequence
<220>
<223> Contains the cleavage site for the restriction endonuclease BamHI
<400> 8
                                                                     29
cgggatcccg ctcacaagcc cgagtagga
<210> 9
<211> 353
<212> PRT
<213> Homo sapiens
<400> 9
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Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile 115 120 125

Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His 130 135 140

Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile Cys 145 150 155 160

Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu Leu 165 170 175

Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr Glu 180 185 190

Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile Leu 195 200 205

Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe Cys 210 215 220

Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys 225 230 235 240

His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu 245 250 255

Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg 260 265 270

Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn.His Ile Asp Arg  $275 \hspace{1.5cm} 280 \hspace{1.5cm} 285 \hspace{1.5cm}.$ 

Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu Asn 290 295 300

Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu Leu 305 310 315 320

Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro Lys 325 330 335

Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser Thr 340 345 350

Thr

### IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Li Attorney Docket No.: PF218US

Application Serial No.: 09/101,518 Art Unit: 1646

Filed: January 11, 1996 Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

#### **DECLARATION OF MELANIE LENHART UNDER 37 C.F.R. § 1.132**

I, Melanie Lenhart, hereby declare and state as follows:

- 1. I am employed by Human Genome Sciences, Inc. ("HGS"), Rockville, Maryland, as a Manager in the PreClinical Discovery department. Since I began working at HGS in 1995, my duties have primarily included carrying out and analyzing, as both a bench scientist and a manager, extensive DNA sequencing.
- 2. A partially redacted copy of the American Type Culture Collection

  ("ATCC") deposit receipt for Deposit Number 97334 is attached hereto as Exhibit A. As the deposit receipt indicates, ATCC Deposit Number 97334 contains a DNA plasmid assigned to the HGS Code Number 498,333, also known within HGS as HGS Clone ID HSATU68. I requested from the ATCC a sample of ATCC Deposit Number 97334 by a purchase order numbered 81449 dated March 13, 2001, a copy of which is attached hereto as Exhibit B. I received the sample of ATCC Deposit Number 97334 from the ATCC in April of 2001, as evidenced by Sales Order # S0241638 from the ATCC, a copy of which is attached hereto as Exhibit C.
- 3. I have been shown what has been presented to me as Figures 1A-1D as originally filed in the above-captioned patent application (hereinafter "original Figures

1A-1D"), a copy of which original Figures 1A-1D is attached hereto as Exhibit D. I used the nucleotide sequence of HSATU68, as shown in original Figures 1A-1D, as a reference to compare to the nucleotide sequence of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334.

- 4. A sample of ATCC Deposit Number 97334 was thoroughly sequenced under my supervision in my laboratory at HGS using sequencing methods which were routine and well known in the art prior to January 11, 1996. Exhibit E depicts an alignment of the nucleotide sequence of the deposited clone with the nucleotide sequence shown in original Figures 1A-1D.
- 5. The nucleotide sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at position 491. More particularly, original Figures 1A-1D show an A residue at position 491, while a T residue is present in the sequence obtained from the DNA clone contained in ATCC Deposit Number 97334.
- 6. As a result of the above difference at position 491 of the nucleotide sequence, the encoded amino acid sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at the 107th codon. More particularly, the 107th codon of the nucleotide sequence in original Figures 1A-1D shows an AAC, encoding for an Asn, which differs from the TAC sequence, encoding for a Tyr, deduced from the DNA clone contained in ATCC Deposit Number 97334.
- 7. The differences in the nucleotide and encoded amino acid sequences noted in paragraphs 5-6 above have been adjusted in the version of Figures 1A-1D attached hereto as Exhibit F. Exhibit G is a marked up version of original Figures 1A-1D showing in red ink the changes made. The nucleotide sequence shown in Exhibit G is identical at

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all but one nucleotide to that shown in original Figures 1A-1D; the amino acid sequence shown in Exhibit F is identical at all but one amino acid residue to that shown in original Figures 1A-1D, with the same start codon, stop codon, and length.

- 8. Based on the experiments described above and the high degree of similarity between the nucleotide and amino acid sequences of original Figures 1A-1D and the corresponding sequences of the deposited clone as shown in Exhibits E, it is my belief that a person of ordinary skill in the art, upon routine sequencing of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334 using methods well known in the art prior to January 11, 1996, would readily determine that the residue at position 491 is an A residue; and thus, the encoded amino acid at position 107 is Tyr, especially when using original Figures 1A-1D as a guide.
- 9. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application captioned above or any patent issuing thereupon.

Date: 3/14/02 Molarie Lephort